

Figure 1

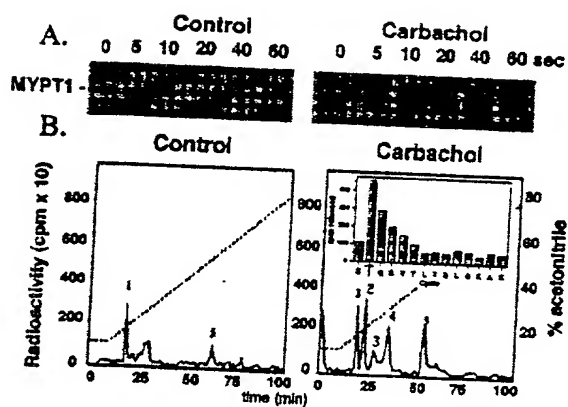


Figure 2

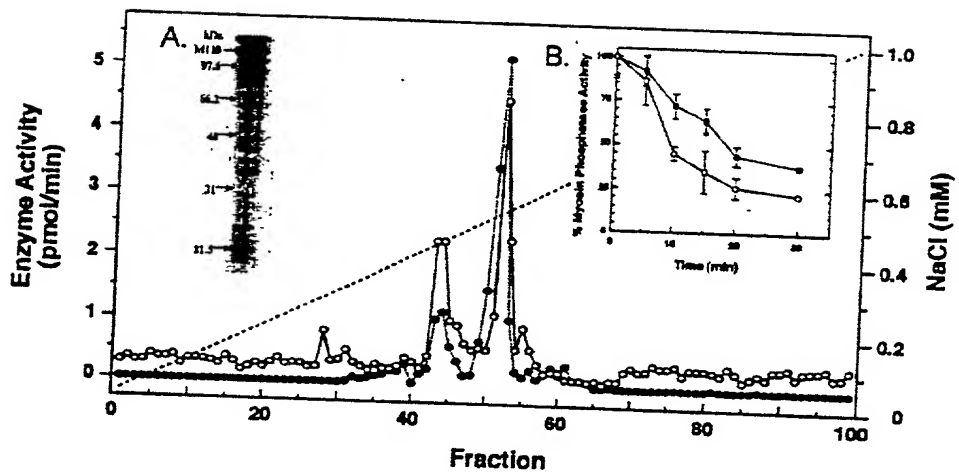
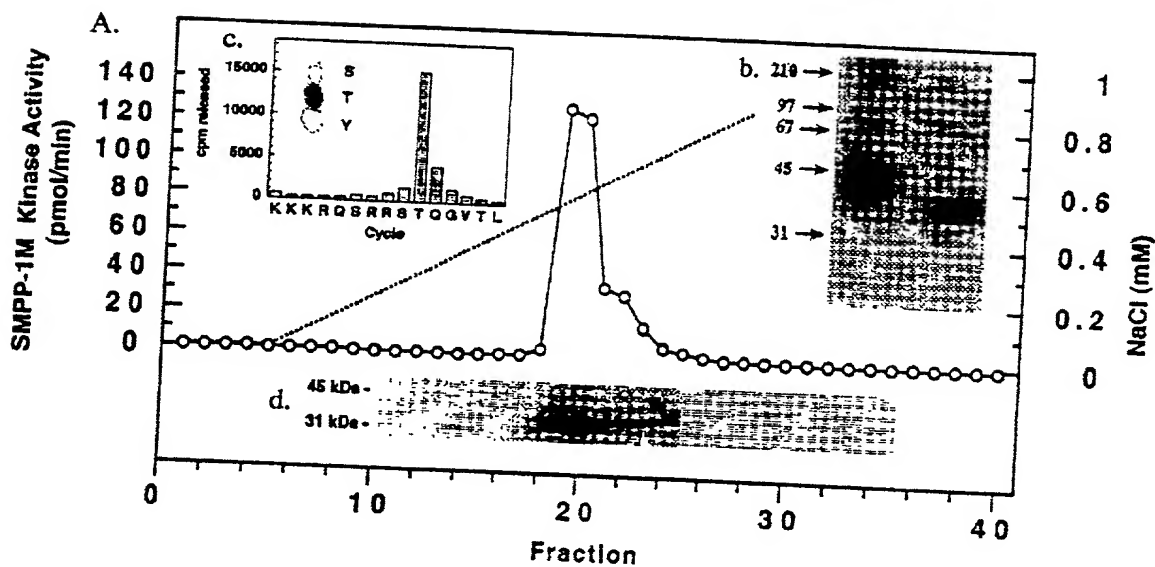


Figure 3



Edman cycle number	Amino acids recovered at each cycle	FASTA Aligned Sequence	Called Protein
		MDRELGGQFAIV-----	
1.	M M M M	MSYFQEDVEDRYEMGELGGQFAIVKCKQKQTKYAAKFKERPLSSRRGVSKKIZREVMILREIRKPNITLW	
2.	E I L V	10 20 30 40 50 60 70 80	
3.	A T D E	-----MLDXXIFKRPDQ-----	
4.	Q K L X		
5.	N R G V	DI FENATDVVLLLELVSGGELFQFLAEKSSLTIDETQFLQILDGVHYLSEKRIANFELKPNIMLLDNVFNPRIKLI	/IP
6.	I S L A	90 100 110 120 130 140 150 160	kinase
7.	V F C K	-----	
8.	Q Y L V		
9.	R K F V	DFGIANKIKAGMEFKNIPOTPEFVAPETVMYSPGLGADNMSIGVITYILLGASPFLEGTQETLTNIGAVHYDFDEY	
10.	A S T E	170 180 190 200 210 220 230 240	
11.	T G C	-----MTIAQLKDKXIX-----	
12.	V E Q A	MSSTSELAKQFIRLLVDFKRNMTIAGSLGHWIKVWSPEDGAKKPERNELAAALAEYHLESNSWPNSTSYASERP	
		250 260 270 280 290 300 310 320	

Figure 4

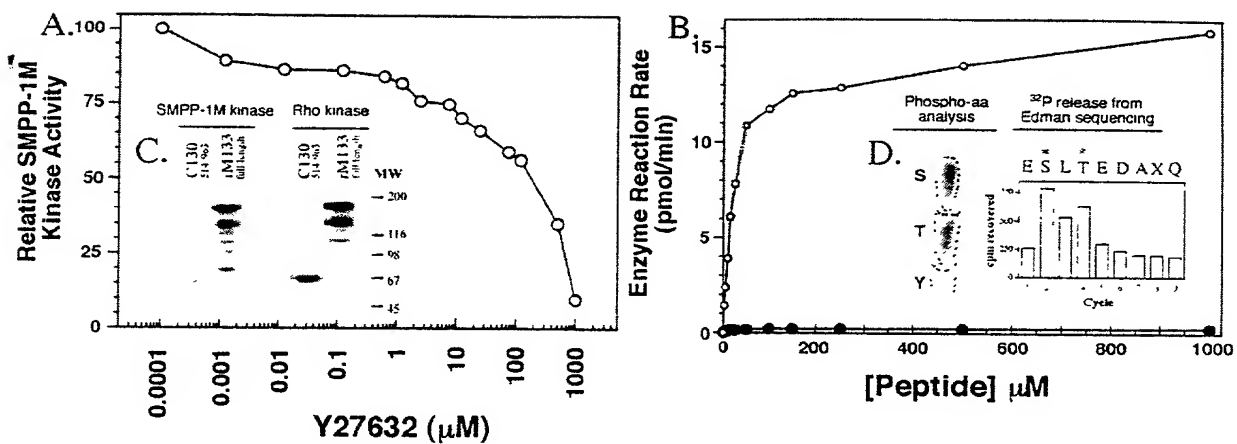
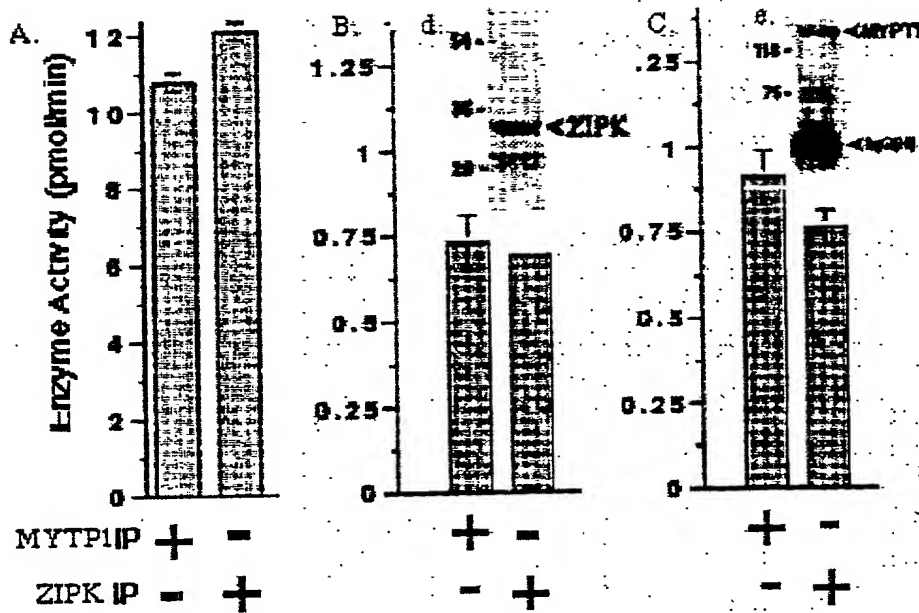


Figure 5

Figure 6



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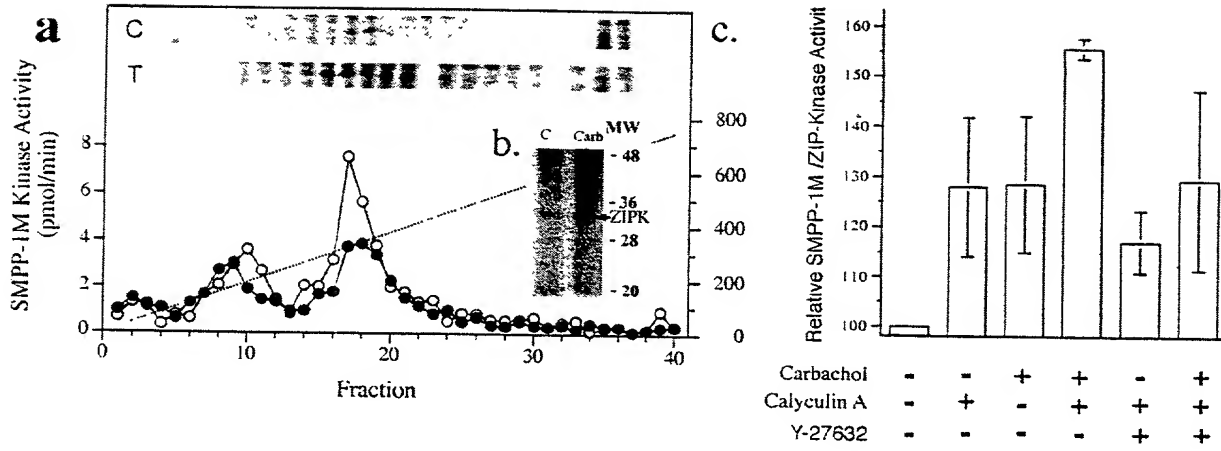


Figure 7

Figure 8

Putative nucleotide sequence of smooth muscle MYPT-kinase showing start site in bold.

GNT AT GNATA	TCGGTTTAAT	CGGCCGGAGC	TCGCCCNCNG	GGCAGCTGGA	
CTCCCTCTCA	GACCTCCTTC	TTTCTCGCCC	TCAGCACGGG	ATTAACCTCA	100
CTTGACTGTT	CTTGGGTCCC	CGGTGCCGGG	CCAGCGTCCT	CTCCCTCAAG	150
GCAATCCCCA	AGTGTCTGTC	ATGAGGCTCT	TTGGGCAGTT	CTGTTGTTGT	200
GGGAAACCTG	GGAACAGATG	CACAGAGGCT	GGGGTACAGA	GTCCTGCCTT	250
CCTCTGGGTC	TGCAGCGCTT	AGCTGTTCTT	TCCCCACAG	CGGCCAGTTC	300
GCCATCGTGC	GCAAGTGCCA	GCAGAAGGGC	ACCGGCATGG	AGTACGCGGC	350
CAAGTTCATA	AAGAAGCGGC	GCCTGCCGTC	CAGCCGGCGC	GGTGTGAGCC	400
GTGAGGAGAT	CGAGCGCGAG	GTGAGCATCC	TGCGCGAGAT	CCGCCACCCC	450
AACATCATCA	CGCTGCACGA	TGTGTTTCGAG	AACAAGACAG	ATGTGGTGCT	500
GATCTTGGAG	CTGGTGTCCG	GCGGCGAACT	TTTCGACTTT	CTGGCTGAGA	550
AGGATCACTG	ACAGAGGATG	AGGCCACGCA	GTTCTCTAAG	CAGATCCTGG	600
ACGGTGTCCA	CTACCTGCAC	TCCAAGCGCA	TCGCGCACTT	TGACCTGAAG	650
CCGGAGAACA	TCATGTTGCT	GGACAAGCAT	GCAGCCAGCC	CACGCATTAA	700
GCTCATCGAC	TTTGGCATCG	CGCACAGGAT	CGAGGCCGGT	AGCGAGTTCA	750
AGAACATCTT	TGGCACGCCA	GAGTTCGTCT	GTGAGGGGCA	GGTGTGGGCA	800
CCACCCGATA	GGGTAGATTT	TGCACGGCCT	TGGCCTGACC	TGCCTCAACA	850
ATCCTGTCTT	CCACAGCCCC	TGAGATTGTA	AACTATGAAC	CACTTGGCTT	900
GGAAGCTGAT	ATGTGGAGCA	TCGGCGTCAT	CACCTACATC	CTGTGAGTGC	950
CTGAGATGGG	CAGGGGCCTC	AGACTGTACC	TGCTAGAGGC	CCAGGGATCA	1000
GGGCTGGCAC	CTCTGCAAAC	TGCAAACACT	GGGGCTGAGA	GATGTCCCTG	1050
GGAACNCTGG	ATATGCCTGG	GCCCCACCAA	NGTAGGACCA	TNC	1093

Figure 9

Deduced amino acid sequence of rat aorta smooth muscle MYPT-kinase (underlined shows alignment with 52kDa ZIP kinase sequence)

XXIIGLIGRS SPXGQLDSL DILLSRPQHG INLT*LFLGP RCRASVLSLK
AIPKCLS*GS LGSSVVVGNL GTDAQRLGYR VLPSSGSAAL SCSFPHSGOF
AIVRKCOOKG TGMEXAAKEI KKRRLPSSRR GVSREEIERE VSILREIRHP
NIITLHDVFE NKIDVVILE LVSGGELEDF LAEKDH*QRM RPRSSSSRSW
TVSTTCTPSA SRTLT*SRRT SCCWTSMQPA HALSSSTLAS RTGSRPVASS
RTSLARQSSS VRGRCGHPPI G*ILHGLGLT CLNNPVFHSP *DCKL*TTWL
GS*YVEHRRH HLHPVSA*DG QGPQTVPARG PGIRAGTSAN CKHWG*EMSL
GTLDMPGPHQ XRTX